	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplas reticulu
0	Q02952	AKA12_HUMAN	Homo sapiens	A-kinase anchor protein 12	20.485228	S1132;S1133;T1440;T1443	S11;S19;S28;S75;S96;S154;S219;S248;S258;S280;S283;S286;S347;S371;T374;S381;S392;S483;S505;S554;S557;S598;S612;S627;S629;T642;S644;S645;S648;S651;S696;S697;S698;S749;S761;S787;S806;S1328;S1331;S1391;S1395;S1587;S1727	26853435;23301498;38253038;38665916	MGAGSSTEQRSPEQPPEGSSTPAEP EPSGGGPSAEAAPDTTADPAIAASDP ATKLLQKNGQLSTINGVAEQDELSL QEGDLNGQKGALNGQGALNSQEEE EVIVTEVGQRDSEDVSKRDSDKEMA TKSAVVHDITDDGQEETPEIIEQIPSS ESNLEELTQPTESQANDIGFKKVFK FVGFKFTVKKDKTEKPDTVQLLTVK KDEGEGAAGAGDHKDPSLGAGEAA SKESEPKQSTEKPEETLKREQSHAEI SPPAESGQAVEECKEEGEEKQEKEP SKSAESPTSPVTSETGSTFKKFFTQG WAGWRKKTSFRKPKEDEVEASEKK KEQEPEKVDTEEDGKAEVASEKLTA SEQAHPQEPAESAHEPRLSAEYEKV ELPSEEQVSGSQGPSEEKPAPLATEV FDEKIEVHQEEVVAEVHVSTVEERT EEQKTEVEETAGSVPAEELVEMDAE PQEAEPAKELVKLKETCVSGEDPTQ GADLSPDEKVLSKPPEGVVSEVEML SSQERMKVQGSPLKKLFTSTGLKKL SGKKQKGKRGGGDEESGEHTQVPA DSPDSQEEQKGESSASSPEEPEEITC LEKGLAEVQQDGEAEEGATSDGEKK REGVTPWASFKKMVTPKKRVRRPSE SDKEDELDKVKSATLSSTESTASEM QEEMKGSVEEPKPEEPKRKVDTSVS WEALICVGSSKKRARRGSSSDEEGG PKAMGGDHQKADEAGKDKETGTDG ILAGSQEHDPGQGSSSPEQAGSPTE GEGVSTWESFKRLVTPRKKSKSKLE EKSEDSIAGSGVEHSTPDTEPGKEES WVSIKKFIPGRRKKRPDGKQEQAPV EDAGPTGANEDDSDVPAVVPLSEYD AVEREKMEAQQAQKSAEQPEQKAA TEVSKELSESQVHMMAAAVADGTR AATIIEERSPSWISASVTEPLEQVEAE AALLTEEVLEREVIAEEEPPTVTEPLP ENREARGDTVVSEAELTPEAVTAAE TAGPLGAEEGTEASAAEETTEMVSA VSQLTDSPDTTEEATPVQEVEGGVP DIEEQERRTQEVLQAVAEKVKEESQ LPGTGGPEDVLQPVQRAEAERPEEQ AEASGLKKETDVVLKVDAQEAKTEP FTQGKVVGQTTPESFEKAPQVTESIE SSELVTTCQAETLAGVKSQEMVMEQ AIPPDSVETPTDSETDGSTPVADFDA PGTTQKDEIVEIHEENEVASGTQSG GTEAEAVPAQKERPPAPSSFVFQEET KEQSKMEDTLEHTDKEVSVETVSIL SKTEGTQEADQYADEKTKDVPFFEG LEGSIDTGITVSREKVTEVALKGEGT EEAECKKDDALELQSHAKSPPSPVE REMVVQVEREKTEAEPTHVNEEKLE HETAVTVSEEVSKQLLQTVNVPIIDG AKEVSSLEGSPPPCLGQEEAVCTKIQ VQSSEASFTLTAAAEEEKVLGETANI LETGETLEPAGAHLVLEEKSSEKNE DFAAHPGEDAVPTGPDCQAKSTPVI VSATTKKGLSSDLEGEKTTSLKWKS DEVDEQVACQEVKVSVAIEDLEPEN GILELETKSSKLVQNIIQTAVDQFVR TEETATEMLTSELQTQAHVIKADSQ DAGQETEKEGEEPQASAQDETPITS AKEESESTAVGQAHSDISKDMSEAS EKTMTVEVEGSTVNDQQLEEVVLPS EEEGGGAGTKSVPEDDGHALLAERI EKSLVEPKEDEKGDDVDDPENQNS ALADTDASGGLTKESPDTNGPKQKE KEDAQEVELQEGKVHSESDKAITPQ AQEELQKQERESAKSELTES	None	None	None	None	None	None